



11/11

SEQUENCE LISTING

<110> Saltveit, Michael E.
Campos, Reinaldo
Nonogaki, Hiroyuki
Suslow, Trevor
The Regents of the University of California

<120> Characterization of Phenylalanine Ammonia-Lyase (PAL)
Gene in Wounded Lettuce Tissue

<130> 023070-124500US

<140> US 09/964,992

<141> 2001-09-26

<150> US 60/235,956

<151> 2000-09-26

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<170> PatentIn Ver. 2.1

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<212> PRT

<213> Lactuca sativa

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35 40 45

Val Lys Leu Gly Gly Glu Thr Leu Thr Val Ser Gln Val Ala Gly Ile
50 55 60

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65 70 75 80

Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met
85 90 95

Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr
100 105 110

Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile
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Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Thr Ser His
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Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met Ile Val Arg Ile Asn
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Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Ala
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Ile Thr Lys Phe Leu Asn Asn Asn Ile Thr Pro Cys Leu Pro Leu Arg
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Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala
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Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys
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Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro
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Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ser Ser Thr Lys Met
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Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val
370 375 380

Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe Gln Gly Thr Pro Ile
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Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys
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Gly Phe Lys Gly Gly Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu
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Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln
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His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr
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580 585 590

Val Asp His Ala Leu Asn Asn Gly Glu Thr Glu Lys Asn Thr Asn Thr
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Leu Ser Ile Pro Asn Arg Ile Lys Ala Cys Arg Ser Tyr Pro Leu Tyr
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Val Thr Ser Pro Gly Glu Glu Phe Asp Arg Val Phe Thr Ala Met Cys
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35 40 45

Glu Phe Arg Lys Pro Val Val Arg Leu Gly Gly Glu Thr Leu Thr Val
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Ser Gln Val Ala Ala Ile Ala Ser Asp Asn Ala Gly Val Lys Val
65 70 75 80

Glu Leu Ser Glu Thr Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp
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Val Met Glu Ser Met Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr
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Gly Phe Gly Ala Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu
115 120 125

Gln Lys Glu Leu Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly
130 135 140

Thr Glu Ser Thr His Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met
145 150 155 160

Leu Val Arg Ile Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe
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Glu Ile Leu Glu Ala Ile Thr Lys Phe Leu Asn His Asn Val Thr Pro
180 185 190

Phe Leu Pro Leu Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro
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Leu Ser Tyr Ile Ala Gly Leu Leu Thr Gly Arg Ala Asn Ser Lys Ala
210 215 220

Val Gly Pro Thr Gly Glu Val Leu Asn Ala Glu Lys Ala Phe Ala Glu
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Ala Gly Val Glu Gly Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu
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Ala Leu Val Asn Gly Thr Ala Val Gly Ser Gly Met Ala Ser Met Val
260 265 270

Leu Phe Asp Ala Asn Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala
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Ile Phe Ala Glu Val Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu
290 295 300

Thr His Lys Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ala Ile
305 310 315 320

Met Glu Tyr Ile Leu Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys
325 330 335

Val His Glu Met Asp Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala
340 345 350

Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg
355 360 365

Ser Ser Thr Lys Met Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn
370 375 380

Pro Leu Ile Asp Val Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe
385 390 395 400

Gln Gly Thr Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile
405 410 415

Ala Ala Ile Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn
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Asp Phe Tyr Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn
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Pro Ser Leu Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser
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Tyr Cys Ser Glu Leu Gln Phe Leu Ala Asn Pro Val Thr Asn His Val
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Gln Ser Ala Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile
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Ser Ala Arg Lys Thr Ala Glu Ser Val Glu Ile Leu Lys Leu Met Ser
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Thr Thr Tyr Leu Val Ala Leu Cys Gln Ser Ile Asp Leu Arg His Leu
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Glu Glu Asn Leu Lys Ser Thr Val Lys Asn Thr Val Ser Leu Val Ala
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Lys Lys Ile Leu Thr Thr Gly Val Asn Gly Glu Leu His Pro Ser Arg
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Phe Cys Glu Lys Asp Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe
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Ala Tyr Ile Asp Asp Ala Cys Ser Ala Thr Tyr Pro Leu Met Gln Lys
580 585 590

Leu Arg Gln Val Ile Val Asp His Ala Leu Asn Asn Glu Asn Asp Ala
595 600 605

Gly Thr Ser Ile Phe Gln Lys Ile Ser Glu Phe Glu Glu Leu Lys
610 615 620

Ala Val Leu Pro Lys Glu Val Glu Gly Val Arg Ser Ala Tyr Glu Ser
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Ser Thr Leu Thr Ile Pro Asn Arg Ile Lys Glu Cys Arg Ser Tyr Pro
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Leu Tyr Arg Phe Val Arg Glu Glu Leu Gly Thr Gly Phe Leu Thr Gly
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Glu Glu Val Thr Ser Pro Gly Glu Glu Phe Asp Lys Val Phe Thr Ala
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Trp Asn Gly Val Pro Leu Pro Ile Ser
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Val Lys Leu Gly Gly Glu Thr Leu Thr Val Ser Gln Val Ala Gly Ile
50 55 60
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65 70 75 80
Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met
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Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr
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Ser His Arg Arg Thr Lys Asn Gly Gly Ala Leu Gln Lys Glu Leu Ile
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145 150 155 160
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Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala Val Gly Pro Ala Gly
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Glu Val Leu Asn Ala Glu Ser Ala Phe Ala Gln Ala Gly Val Glu Gly
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Thr Ala Val Gly Ser Gly Met Ala Ser Met Val Leu Phe Glu Ala Asn
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Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val
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His His Pro Gly Gln Ile Glu Ala Ala Ile Met Glu Tyr Ile Leu
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Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys Val His Glu Met Asp
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370 375 380

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Gly Leu Pro Ser His Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Ser
435 440 445

Gly Phe Lys Gly Gly Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu
450 455 460

Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln
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His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr
485 490 495

Ala Glu Ala Val Asp Ile Leu Lys Leu Met Ser Ser Thr Tyr Leu Val
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Ala Leu Cys Gin Ser Ile Asp Leu Arg His Leu Glu Glu Asn Met Lys
515 520 525

Ser Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Lys Val Leu Thr
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Met Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys Asp
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Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Ala Asp Asp
565 570 575

Pro Cys Leu Thr Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val Leu
580 585 590

Val Asp His Ala Leu Asn Asn Gly Glu Thr Glu Lys Asn Ala Asn Thr
595 600 605

Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Asp Glu Leu Lys Ala Ile
610 615 620

Leu Pro Lys Glu Val Glu Ser Val Arg Val Ala Phe Glu Asn Gly Thr
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<211> 17

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17

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<221> modified_base

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<223> n = g, a, c or t

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rice (*Oryza sativa*), or wheat (*Triticum aestivum*)

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<223> Description of Artificial Sequence:PAL conserved
region peptide fragment from sunflower (*Helianthus*
annuus), *Arabidopsis thaliana*, parsley
(*Petroselinum crispum*), carrot (*Daucus carota*),
tobacco (*Nicotiana tabacum*), rice (*Oryza sativa*),
or wheat (*Triticum aestivum*)

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His Gly Gly Asn Phe Gln Gly
1 5

<210> 10
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peptide fragment

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23

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23